**Table 2**. GO annotation results of the DEGs from 50 tumor and 61 adjacent non-tumor tissues of PDAC patients. **A,** **Down‑regulated**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Category | Term/gene function | count | % | P‑value | Genes |
|  |  |  |  |  |  |
| GOTERM\_BP | GO:0021942~radial glia guided migration of Purkinje cell | 2 | 1.0929 | 0.02125823 | DAB1, CTNNA2 |
| GOTERM\_BP | GO:0021756~striatum development | 2 | 1.0929 | 0.0461805 | CNTNAP2, SLITRK5 |
| GOTERM\_BP | GO:0016311~dephosphorylation | 3 | 1.6393 | 0.05261072 | ALPP, PON1, LPIN1 |
| GOTERM\_BP | GO:0060134~prepulse inhibition | 2 | 1.0929 | 0.05434804 | FABP7, CTNNA2 |
| GOTERM\_BP | GO:0007409~axonogenesis | 3 | 1.6393 | 0.06623069 | SLITRK5, KERA, CTNNA2 |
| GOTERM\_MF | GO:0005261~cation channel activity | 2 | 1.09290 | 0.09604912 | CATSPER3, TRPM6 |
| GOTERM\_CC | GO:0014069~postsynaptic density | 4 | 2.18579 | 0.04441086 | DAB1, MAP1B, CTNNA2, MT3 |
| GOTERM\_CC | GO:0043025~neuronal cell body | 5 | 2.73224 | 0.04615778 | CNTNAP2, DAB1, KLHL14, FABP7, RACK1 |
| GOTERM\_CC | GO:0005615~extracellular space | 11 | 6.01093 | 0.06080918 | OLFM3, PON1, IFNK, KRT78, SOSTDC1, GAST, KERA, PXDNL, ANGPTL4, MT3, CPA4 |
| GOTERM\_CC | GO:0043197~dendritic spine | 3 | 1.63934 | 0.06842851 | TENM2, MAP1B, MT3 |
| GOTERM\_CC | GO:0043005~neuron projection | 4 | 2.18579 | 0.08135679 | TENM2, DAB1, KLHL14, STON2 |
| KEGG\_PATHWAY | hsa04670:Leukocyte transendothelial migration | 3 | 1.63934 | 0.08903048 | PLCG2, CTNNA2, BCAR1 |

**B, Up‑regulated**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Category | Term/gene function | count | % | P‑value | Genes |  |
|  |  |  |  |  |  |  |
| GOTERM\_BP | GO:0000184~nuclear-transcribed mRNA catabolic process, nonsense-mediated decay | 16 | 6.80851 | 5.02E-12 | RPL4, RPL30, RPL10, RPLP1, RPS6, RPL8, PNRC2, RPL7A, RPS25, RPL18A, PPP2R1A, PABPC1, RPL39, RPS24, RPS23, RPL19 |  |
| GOTERM\_BP | GO:0006413~translational initiation | 16 | 6.80851 | 3.95E-11 | RPL4, RPL30, RPL10, RPLP1, RPS6, RPL8, EIF1, RPL7A, RPS25, EIF2S3, RPL18A, PABPC1, RPL39, RPS24, RPS23, RPL19 |  |
| GOTERM\_BP | GO:0006614~SRP-dependent cotranslational protein targeting to membrane | 13 | 5.53191 | 6.22E-10 | RPL4, RPL30, RPL10, RPLP1, RPS6, RPL8, RPL7A, RPS25, RPL18A, RPL39, RPS24, RPS23, RPL19 |  |
| GOTERM\_BP | GO:0019083~viral transcription | 13 | 5.53191 | 4.82E-09 | RPL4, RPL30, RPL10, RPLP1, RPS6, RPL8, RPL7A, RPS25, RPL18A, RPL39, RPS24, RPS23, RPL19 |  |
| GOTERM\_BP | GO:0006412~translation | 15 | 6.38298 | 1.08E-06 | RPL4, RPL30, RPL10, RPLP1, RPS6, RPL8, RPL7A, RPS25, RPL18A, SLC25A5, RPL39, RPS24, SLC25A6, RPS23, RPL19 |  |
| GOTERM\_MF | GO:0044822~poly(A) RNA binding | 40 | 17.0213 | 7.38E-11 |  |  |
| GOTERM\_MF | GO:0005515~protein binding | 138 | 58.7234 | 1.59E-10 |  |  |
| GOTERM\_MF | GO:0003735~structural constituent of ribosome | 15 | 6.3830 | 1.41E-07 | RPL4, RPL30, RPLP0P6, RPL10, RPLP1, RPS6, RPL8, RPL7A, RPL18A, SLC25A5, RPL39, RPS24, SLC25A6, RPS23, RPL19 |  |
| GOTERM\_MF | GO:0098641~cadherin binding involved in cell-cell adhesion | 16 | 6.8085 | 6.44E-07 | YWHAE, RAB1A, HSPA8, ANXA1, SND1, RAB10, LIMA1, RPL7A, MYO1B, EIF2S3, SLK, EPCAM, KIF5B, PRDX1, RACK1, SPTBN1 |  |
| GOTERM\_MF | GO:0003723~RNA binding | 19 | 8.0851 | 2.89E-05 | RPL4, DDX18, RPL30, SSB, RPL8, DDX50, QKI, HSP90B1, RPL7A, RPS25, RPL18A, HNRNPH1, HNRNPA2B1, HNRNPD, PDCD4, PABPC1, SRSF5, RPL39, RPL19 |  |
| GOTERM\_CC | GO:0070062~extracellular exosome | 90 | 38.2979 | 7.45E-25 |  |  |
| GOTERM\_CC | GO:0031012~extracellular matrix | 25 | 10.6383 | 6.89E-15 | RPL30, DDX5, PRKDC, ACTG1, HSP90B1, PRDX1, PRSS2, HSPA8, MMP7, BGN, LAMB1, COL1A1, RPS25, COL3A1, MMP14, VCAN, SFRP2, COL1A2, CANX, VIM, P4HB, SLC25A5, GAPDH, FBN1, SLC25A6 |  |
| GOTERM\_CC | GO:0005925~focal adhesion | 27 | 11.4894 | 5.36E-14 | YWHAE, RPL4, RPL30, RPLP1, RPL8, ACTB, ACTG1, HSP90B1, CORO1C, LIMA1, RPL7A, PPP1CC, B2M, JAK1, RPL19, ACTR3, HSPA8, ANXA1, ANXA5, ADAM10, MSN, RAB10, MMP14, ARPC2, VIM, PABPC1, P4HB |  |
| GOTERM\_CC | GO:0016020~membrane | 60 | 25.5319 | 2.68E-12 |  |  |
| GOTERM\_CC | GO:0022625~cytosolic large ribosomal subunit | 10 | 4.2553 | 3.49E-08 | RPL4, RPL7A, RPL30, RPLP0P6, RPL10, RPL18A, RPLP1, RPL8, RPL39, RPL19 |  |
| KEGG\_PATHWAY | hsa03010:Ribosome | 13 | 5.5319 | 2.38E-06 | RPL4, RPL30, RPL10, RPLP1, RPS6, RPL8, RPL7A, RPS25, RPL18A, RPL39, RPS24, RPS23, RPL19 |  |
| KEGG\_PATHWAY | hsa04141:Protein processing in endoplasmic reticulum | 13 | 5.5319 | 2.25E-05 | EDEM3, HSPA8, TRAM1, EIF2AK1, SEL1L, HSP90B1, LMAN1, CANX, DNAJA2, DNAJC10, UBQLN1, SSR1, P4HB |  |
| KEGG\_PATHWAY | hsa05169:Epstein-Barr virus infection | 10 | 4.2553 | 1.87E-04 | USP7, MDM2, HLA-B, PLCG2, HLA-DRA, TNFAIP3, HLA-A, VIM, HLA-G, JAK1 |  |
| KEGG\_PATHWAY | hsa04612:Antigen processing and presentation | 8 | 3.4042 | 2.56E-04 | HSPA8, CD74, CANX, HLA-B, HLA-DRA, HLA-A, B2M, HLA-G |  |
| KEGG\_PATHWAY | hsa05168:Herpes simplex infection | 11 | 4.6808 | 9.22E-04 | CD74, PPP1CC, USP7, EIF2AK1, CSNK2B, HLA-B, HLA-DRA, HLA-A, SRSF5, HLA-G, JAK1 |  |
|  |  |  |  |  |  |  |